

# p-Y694-STAT5A, p-STAT5B dimerizes

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## Introduction

Reactome is open-source, open access, manually curated and peer-reviewed pathway database. Pathway annotations are authored by expert biologists, in collaboration with Reactome editorial staff and cross-referenced to many bioinformatics databases. A system of evidence tracking ensures that all assertions are backed up by the primary literature. Reactome is used by clinicians, geneticists, genomics researchers, and molecular biologists to interpret the results of high-throughput experimental studies, by bioinformaticians seeking to develop novel algorithms for mining knowledge from genomic studies, and by systems biologists building predictive models of normal and disease variant pathways.

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## Literature references

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- Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology*, 14, e1005968. [↗](#)

Reactome database release: 88

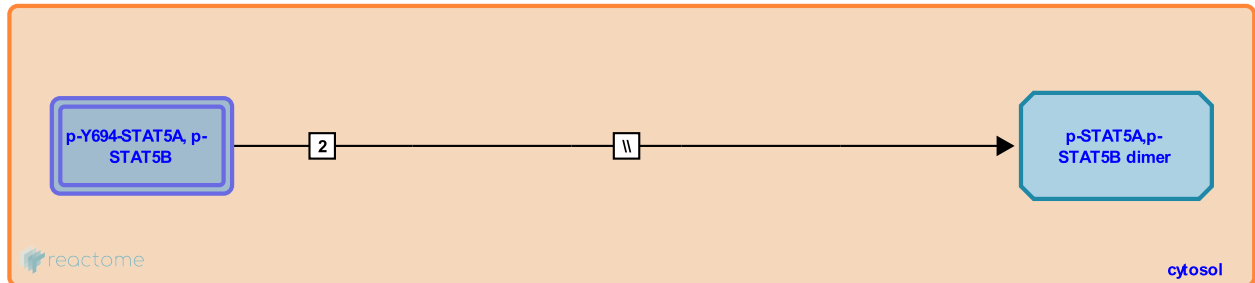
This document contains 1 reaction ([see Table of Contents](#))

## p-Y694-STAT5A, p-STAT5B dimerizes [↗](#)

**Stable identifier:** R-HSA-8985950

**Type:** omitted

**Compartments:** cytosol



Phosphorylated Signal transducer and activator of transcription 5A/B (STAT5) homodimerizes.

Following IL9 induced STAT activation, homodimers of tyrosine phosphorylated STAT5 have been identified (Bauer et al. 1998).

### Literature references

You, Y., Bauer, JH., Lai, SY., Liu, KD., Goldsmith, MA. (1998). Heteromerization of the gammac chain with the interleukin-9 receptor alpha subunit leads to STAT activation and prevention of apoptosis. *J. Biol. Chem.*, 273, 9255-60.

[↗](#)

### Editions

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